

**Figure 1:****ORF of Isocitrate dehydrogenase 1 (XM\_055088)**

(nucleic acid sequence: SEQ ID NO:1; amino acid sequence: SEQ ID NO:2)

5	1	GGC GGC GAA GCG GGG GCA CGC CCT CGC ACA CGC AGA GAT AAA TTG	45
	46	TGC TCC CAT GAC CTT TAT TTG GAA AGT GCC TGC GGG CCT AAA ATT	90
	91	GGC CTT TGT CCC ACC GAG TAC ACT CAG CAC TGT ACT TTA AAC CGG	135
	136	ATA AAC TGG GCT GTC TGG CAG GCG ATA AAC TAC ATT CAG TTG AGT	180
	181	CTG CAA GAC TGG GAG GAA CTG GGG TGA TAA GAA ATC TAT TCA CTG	225
10	226	TCA AGG TTT ATT GAA GTC AAA ATG TCC AAA AAA ATC AGT GGC GGT	270
		M S K K I S G G	8
	271	TCT GTG GTA GAG ATG CAA GGA GAT GAA ATG ACA CGA ATC ATT TGG	315
	9	S V V E M Q G D E M T R I I W	23
	316	GAA TTG ATT AAA GAG AAA CTC ATT TTT CCC TAC GTG GAA TTG GAT	360
15	24	E L I K E K L I F P Y V E L D	38
	361	CTA CAT AGC TAT GAT TTA GGC ATA GAG AAT CGT GAT GCC ACC AAC	405
	39	L H S Y D L G I E N R D A T N	53
	406	GAC CAA GTC ACC AAG GAT GCT GCA GAA GCT ATA AAG AAG CAT AAT	450
	54	D Q V T K D A A E A I K K H N	68
20	451	GTT GGC GTC AAA TGT GCC ACT ATC ACT CCT GAT GAG AAG AGG GTT	495
	69	V G V K C A T I T P D E K R V	83
	496	GAG GAG TTC AAG TTG AAA CAA ATG TGG AAA TCA CCA AAT GGC ACC	540
	84	E E F K L K Q M W K S P N G T	98
	541	ATA CGA AAT ATT CTG GGT GGC ACG GTC TTC AGA GAA GCC ATT ATC	585
25	99	I R N I L G G T V F R E A I I	113
	586	TGC AAA AAT ATC CCC CGG CTT GTG AGT GGA TGG GTA AAA CCT ATC	630
	114	C K N I P R L V S G W V K P I	128
	631	ATC ATA GGT CGT CAT GCT TAT GGG GAT CAA TAC AGA GCA ACT GAT	675
	129	I I G R H A Y G D Q Y R A T D	143
30	676	TTT GTT GTT CCT GGG CCT GGA AAA GTA GAG ATA ACC TAC ACA CCA	720
	144	F V V P G P G K V E I T Y T P	158
	721	AGT GAC GGA ACC CAA AAG GTG ACA TAC CTG GTA CAT AAC TTT GAA	765
	159	S D G T Q K V T Y L V H N F E	173
	766	GAA GGT GGT GGT GTT GCC ATG GGG ATG TAT AAT CAA GAT AAG TCA	810
35	174	E G G G V A M G M Y N Q D K S	188
	811	ATT GAA GAT TTT GCA CAC AGT TCC TTC CAA ATG GCT CTG TCT AAG	855
	189	I E D F A H S S F Q M A L S K	203
	856	GGT TGG CCT TTG TAT CTG GAC ACC AAA AAC ACT ATT CTG AAG AAA	900
	204	G W P L Y L S T K N T I L K K	218
40	901	TAT GAT GGG CGT TTT AAA GAC ATC TTT CAG GAG ATA TAT GAC AAG	945
	219	Y D G R F K D I F Q E I Y D K	233
	946	CAG TAC AAG TCC CAG TTT GAA GCT CAA AAG ATC TGG TAT GAG CAT	990
	234	Q Y K S Q F E A Q K I W Y E H	248
	991	AGG CTC ATC GAC GAC ATG GTG GCC CAA GCT ATG AAA TCA GAG GGA	1035
45	249	R L I D D M V A Q A M K S E G	263
	1036	GGC TTC ATC TGG GCC TGT AAA AAC TAT GAT GGT GAC GTG CAG TCG	1080
	264	G F I W A C K N Y D G D V Q S	278
	1081	GAC TCT GTG GCC CAA GGG TAT GGC TCT CTC GGC ATG ATG ACC AGC	1125
	279	D S V A Q G Y G S L G M M T S	293
50	1126	GTG CTG GTT TGT CCA GAT GGC AAG ACA GTA GAA GCA GAG GCT GCC	1170
	294	V L V C P D G K T V E A E A A	308
	1171	CAC GGG ACT GTA ACC CGT CAC TAC CGC ATG TAC CAG AAA GGA CAG	1215
	309	H G T V T R H Y R M Y Q K G Q	323
	1216	GAG ACG TCC ACC AAT CCC ATT GCT TCC ATT TTT GCC TGG ACC AGA	1260
55	324	E T S T N P I A S I F A W T R	338
	1261	GGG TTA GCC CAC AGA GCA AAG CTT GAT AAC AAT AAA GAG CTT GCC	1305
	339	G L A H R A K L D N N K E L A	353
	1306	TTC TTT GCA AAT GCT TTG GAA GAA GTC TCT ATT GAG ACA ATT GAG	1350
	354	F F A N A L E E V S I E T I E	368
60	1351	GCT GGC TTC ATG ACC AAG GAC TTG GCT GCT TGC ATT AAA GGT TTA	1395
	369	A G F M T K D L A A C I K G L	383

	1396	CCC	AAT	GTG	CAA	CGT	TCT	GAC	TAC	TTG	AAT	ACA	TTT	GAG	TTC	ATG	1440
	384	P	N	V	Q	R	S	D	Y	L	N	T	F	E	F	M	398
	1441	GAT	AAA	CTT	GGA	GAA	AAC	TTG	AAG	ATC	AAA	CTA	GCT	CAG	GCC	AAA	1485
	399	D	K	L	G	E	N	L	K	I	K	L	A	Q	A	K	413
5	1486	CTT	TAA	GTT	CAT	ACC	TGA	GCT	AAG	AAG	GAT	AAT	TGT	CTT	TTG	GTA	1530
	414	L	*														
	1531	ACT	AGG	TCT	ACA	GGT	TTA	CAT	TTT	TCT	GTG	TTA	CAC	TCA	AGG	ATA	1575
	1576	AAG	GCA	AAA	TCA	ATT	TTG	TAA	TTT	GTT	TAG	AAG	CCA	GAG	TTT	ATC	1620
	1621	TTT	TCT	ATA	AGT	TTA	CAG	CCT	TTT	TCT	TAT	ATA	TAC	AGT	TAT	TGC	1665
10	1666	CAC	CTT	TGT	GAA	CAT	GGC	AAG	GGA	CTT	TTT	TAC	AAT	TTT	TAT	TTT	1710
	1711	ATT	TTC	TAG	TAC	CAG	CCT	AGG	AAT	TCG	GTT	AGT	ACT	CAT	TTG	TAT	1755
	1756	TCA	CTG	TCA	CTT	TTT	CTC	ATG	TTC	TAA	TTA	TAA	ATG	ACC	AAA	ATC	1800
	1801	AAG	ATT	GCT	CAA	AAG	GGT	AAA	TGA	TAG	CCA	CAG	TAT	TGC	TCC	CTA	1845
	1846	AAA	TAT	GCA	TAA	AGT	AGA	AAT	TCA	CTG	CCT	TCC	CCT	CCT	GTC	CAT	1890
15	1891	GAC	CTT	GGG	CAC	AGG	GAA	GTT	CTG	GTG	TCA	TAG	ATA	TCC	CGT	TTT	1935
	1936	GTG	AGG	TAG	AGC	TGT	GCA	TTA	AAC	TTG	CAC	ATG	ACT	GGA	ACG	AAG	1980
	1981	TAG	GAG	TGC	AAC	TCA	AAT	GTG	TTG	AAG	ATA	CTG	CAG	TCA	TTT	TTG	2025
	2026	TAA	AGA	CCT	TGC	TGA	ATG	TTT	CCA	ATA	GAC	TAA	ATA	CTG	TTT	AGG	2070
	2071	CCG	CAG	GAG	AGT	TTG	GAA	TCC	GGA	ATA	AAT	ACT	ACC	TGG	AGG	TTT	2115
20	2116	GTC	CTC	TCC	ATT	TTT	CTC	TTT	CTC	CTC	CTG	GCC	TGG	CCT	GAA	TAT	2160
	2161	TAT	ACT	ACT	CTA	AAT	AGC	ATA	TTT	CAT	CCA	AGT	GCA	ATA	ATG	TAA	2205
	2206	GCT	GAA	TCT	TTT	TTG	GAC	TTC	TGC	TGG	CCT	GTT	TTA	TTT	CTT	TTA	2250
	2251	TAT	AAA	TGT	GAT	TTC	TCA	GAA	ATT	GAT	ATT	AAA	CAC	TAT	CTT	ATC	2295
	2296	TTC	TCC			2301											

**Figure 2:****ORF of Isocitrate dehydrogenase 2 (NM\_002168)**

(nucleic acid sequence: SEQ ID NO:3; amino acid sequence: SEQ ID NO:4)

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5      1 ccagcgtagcccgcgccaggcagccggaggagcgcgcgctcggacctctccgc
61 cctgctcgttcgctctccagcttgggtagcgccgctacctcggggtcgtgcgctcgtct
1      1 M A G Y L R V V R S L
121 gcagagcctcaggtcgcggccggcctgggcgcggcgccctgacagccccacctcgc
12 C R A S G S R P A W A P A A L T A P T S
10 181 aagagcagcccgcgccactatgccgacaaaaggatcaaggtggcgaagcccgtggtgg
32 Q E Q P R R H Y A D K R I K V A K P V V
241 agatggatggtgatgagatgaccgtattatctggcagttcatcaaggagaagctcatcc
52 E M D G D E M T R I I W Q F I K E K L I
301 tgccccacgtggacatccagctaaagtattttgacctcgggctcccaaacctgaccaga
15 72 L P H V D I Q L K Y F D L G L P N R D Q
361 ctgatgaccaggtcaccattgactctgactgacctggccacccagaagtacagtggtgtca
92 T D D Q V T I D S A L A T Q K Y S V A V
421 agtggtgccaccatcacccctgatgagcccggtgtggaagagttcaagctgaagaagatgt
112 K C A T I T P D E A R V E E F K L K M
20 481 ggaaaagtcccaatggaactatccggaacatcctgggggggactgtcttcggggagccca
132 W K S P N G T I R N I L G G T V F R E P
541 tcactctgcaaaaacatcccacgcctagtccctggctggaccaagcccatcaccattggca
152 I I C K N I P R L V P G W T K P I T I G
601 ggacgccccatggcgaccagtacaaggccacagactttgtggcagaccggcgccgactt
25 172 R H A H G D Q Y K A T D F V A D R A G T
661 tcaaatggtcttcaccccaaaagatggcagtggtgtcaaggagtggaagtgtacaact
192 F K M V F T P K D G S G V K E W E V N
721 tccccgcaggcgcgctggcatggcatgtacaacaccgacgagtcctctcaggttttg
212 F P A G G V G M G M Y N T D E S I S G F
30 781 cgacagctgttccagtatgccatccagaagaaatggccgctgtacatgagcaccaaga
232 A H S C F Q Y A I Q K K W P L Y M S T K
841 acacatactgaaagcctacgatggcgctttcaaggacatcttcaggagatctttgaca
252 N T I L K A Y D G R F K D I F Q E I F D
901 agcactataagaccgacttcgacaagaataagatctggatgagcaccggctcattgatg
35 272 K H Y K T D F D K N K I W Y E H R L I D
961 acatgggtggctcaggtcctcaagtcttcgggtggctttgtgtgggctgcaagaactatg
292 D M V A Q V L K S S G G F V W A C K N Y
1021 acggagatgtgcagtcagacatcctggcccagggttttggtcccttgccctgatgacgt
312 D G D V Q S D I L A Q G F G S L G L M T
40 1081 ccgtcctggtctgccctgatgggaagacgattgaggctgaggccgctcatgggaccgtca
332 S V L V C P D G K T I E A E A A H G T V
1141 cccgccactatcgggagcaccagaaggcgccgcccaccagcaccaaccccatcgccagca
352 T R H Y R E H Q K G R P T S T N P I A S
1201 tctttgcctggacacgtggcctggagcaccgggggaagctggatgggaaccaagacctca
45 372 I F A W T R G L E H R G K L D G N Q D L
1261 tcaggtttgcccagatgctggagaaggtgtgctggagacggtggagagtggagccatga
392 I R F A Q M L E K V C V E T V E S G A M
1321 ccaaggacctggcggtgctcattcacggcctcagcaatgtgaagctgaacgagcacttcc
412 T K D L A G C I H G L S N V K L N E H F
50 1381 tgaacaccacggacttcctcgacaccatcaagagcaacctggacagagccctgggcaggc
432 L N T T D F L D T I K S N L D R A L G R
1441 agtagggggaggcgccaccatggctgcagtggaggggcccagggtgagccggcggtcc
452 Q *
1501 tcctgagcgcgccagaggggtgagcctcacagccctctctggaggcctttctaggggatg
1561 tttttttataagccagatgttttttaaagcatatgtgtgtttccctcatggtgacgtga
1621 ggcaggagcagtgcggttttacctcagccagtcagtatgttttgatactgtaatttatat
1681 tgcccttggaacacatggtgccatatttagctactaaaaagctcttcacaaaaaaaaaa

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Applicants: Paz Einat et al.

U.S. Serial No.: Not Yet Known

Filing Date: July 11, 2003

Title: ISOCITRATE DEHYDROGENASE AND  
USES THEREOF

3 of 12

**Figure 3:****Isocitrate dehydrogenas anti sense fragment**

(SEQ ID NO: 5)

5 5' TGCTCTGTGGGCTAACCCCTCTGGTCCAGGCAAAAATGGAAGCAATGGGATTGGTGGACGTCTCCTGT  
CCTTTCTGGTACATGCGGTAGTGACGGGTACAGTCCCGTGGGCAGCCTCTGCTTCTACCGTCTTGCCA  
TCTGGACAAACCAGCACGCTGGTCATCATGCCGAGAGAGCCATACCCTTGGGCCACAGAGTCCGACTGC  
ACGTCACCATCATAGTTTTTACAGGCCCAGATGAAGCCTCCCTCTGATCTCATAGCTGGGGCCACCATG  
10 TCGTCGATGAGCCTATGCTCATAACAGATCTTTTGAGCTTCAAACCTGGGACTTGACTGCTTGTCATAT  
ATCTCCTGAAAGATGTCTTTAAAACGCCCATCATATTTCTTCAGAATGGTGTTTTTGGTGCTCAGATAC  
AAAGGCCAACCCCTTAGACAGAGCCATTTGGAAGGAAGTGTGTGCAAAATCTTCAATTGACTTATCTTGA  
TTATACATCCCCATGACAACACCACCACCTTCTTCAAGTTATGTACCAGG' 3

**Figure 4:**

**IDH siRNA sequence**

(SEQ ID NO:6)

5 5' AATCGTGATGCCACCAACGAC '3

**Figure 5:**

**Alignment between Isocitrate dehydrogenase 1 (XM\_055088) and AS fragment**

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5   ICD      1   GGCGGCGAAGCGGGGGCAGCCCTCGCACACGCAGAGATAAATTGTGCTCCCATGACCTT
   IRT-4C1  1   -----

   ICD      61   TATTTGGAAAGTGCCTGCGGGCCTAAAATTGGCCTTTGTCCCACCGAGTACACTCAGCAC
   IRT-4C1  1   -----

10  ICD      121  TGTACTTTAAACCGGATAAACTGGGCTGTCTGGCAGGCGATAAACTACATTCAGTTGAGT
   IRT-4C1  1   -----

   ICD      181  CTGCAAGACTGGGAGGAACTGGGGTGATAAGAAATCTATTCACTGTCAAGGTTTATTGAA
   IRT-4C1  1   -----

15  ICD      241  GTCAAAATGTCCAAAAAATCAGTGGCGGTTCTGTGGTAGAGATGCAAGGAGATGAAATG
   IRT-4C1  1   -----

   ICD      301  ACACGAATCATTTGGGAATTGATTAAAGAGAAACTCATTTTCCCTACGTGGAATTGGAT
   IRT-4C1  1   -----

   ICD      361  CTACATAGCTATGATTTAGGCATAGAGAATCGTGATGCCACCAACGACCAAGTCACCAAG
   IRT-4C1  1   -----

25  ICD      421  GATGCTGCAGAAGCTATAAAGAAGCATAATGTTGGCGTCAAATGTGCCACTATCACTCCT
   IRT-4C1  1   -----

   ICD      481  GATGAGAAGAGGGTTGAGGAGTTCAAGTTGAAACAAATGTGGAAATCACCAAATGGCACC
   IRT-4C1  1   -----

30  ICD      541  ATACGAAATATTCTGGGTGGCACGGTCTTCAGAGAAGCCATTATCTGCAAAAATATCCCC
   IRT-4C1  1   -----

   ICD      601  CGGCTTGTGAGTGGATGGGTAAAACCTATCATCATAGGTCGTCATGCTTATGGGGATCAA
   IRT-4C1  1   -----

   ICD      661  TACAGAGCAACTGATTTTGTGTCTCTGGGCCTGGAAAAGTAGAGATAACCTACACACCA
   IRT-4C1  1   -----

40  ICD      721  AGTGACGGAACCCAAAAGGTGACATACTGGGTACATAACTTTGAAGAAGGTGGTGGTGT
   IRT-4C1  1   -----CTGGGTACATAAC--TTGAAGAAGGTGGTGGTGT

   ICD      781  GGCATGGGGATGTATAATCAAGATAAGTCAATTGAAGATTTTGCACACAGTTCCTTCCAA
   IRT-4C1  34  GTCATGGGGATGTATAATCAAGATAAGTCAATTGAAGATTTTGCACACAGTTCCTTCCAA

   ICD      841  ATGGCTCTGTCTAAGGGTTGGCCTTTGTATCTGAGCACCAAAAACACTATTCTGAAGAAA
   IRT-4C1  94  ATGGCTCTGTCTAAGGGTTGGCCTTTGTATCTGAGCACCAAAAACACCATTCTGAAGAAA

50  ICD      901  TATGATGGGCGTTTTAAAGACATCTTTCAGGAGATATATGACAAGCAGTACAAGTCCCAG
   IRT-4C1  154  TATGATGGGCGTTTTAAAGACATCTTTCAGGAGATATATGACAAGCAGTACAAGTCCCAG

   ICD      961  TTTGAAGCTCAAAAGATCTGGTATGAGCATAGGCTCATCGACGACATGGTGGCCCCAAGCT
   IRT-4C1  214  TTTGAAGCTCAAAAGATCTGGTATGAGCATAGGCTCATCGACGACATGGTGGCCCCAGCT

55  ICD      1021  ATGAAATCAGAGGGAGGCTTCATCTGGGCCTGTAAAACTATGATGGTGACGTGCAGTCG
   IRT-4C1  274  ATGAGATCAGAGGGAGGCTTCATCTGGGCCTGTAAAACTATGATGGTGACGTGCAGTCG

   ICD      1081  GACTCTGTGGCCCAAGGGTATGGCTCTCTCGGCATGATGACCAGCGTGCTGGTTTGTCCA
   IRT-4C1  334  GACTCTGTGGCCCAAGGGTATGGCTCTCTCGGCATGATGACCAGCGTGCTGGTTTGTCCA

60  ICD      1141  GATGGCAAGACAGTAGAAGCAGAGGCTGCCACGGGACTGTAACCCGTCACTACCGCATG
   IRT-4C1  394  GATGGCAAGACGGTAGAAGCAGAGGCTGCCACGGGACTGTAACCCGTCACTACCGCATG

65  ICD      1201  TACCAGAAAGGACAGGAGACGTCCACCAATCCCATTGCTTCCATTTTGCCTGGACCAGA

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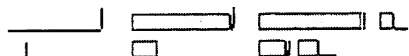
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	ICD	1261	GGGTTAGCCACAGAGCAAGCTTGATAACAATAAAGAGCTTGCCTTCTTTGCAAATGCT
5	IRT-4C1	514	GGGTTAGCCACAGAGCA-----
	ICD	1321	TTGGAAGAAGTCTCTATTGAGACAATTGAGGCTGGCTTCATGACCAAGGACTTGGCTGCT
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10	ICD	1381	TGCATTAAAGGTTTACCCAATGTGCAACGTTCTGACTACTTGAATACATTTGAGTTCATG
	IRT-4C1	531	-----
	ICD	1441	GATAAACTTGGAGAAAACCTGAAGATCAAACCTAGCTCAGGCCAAACTTTAAGTTCATACC
	IRT-4C1	531	-----
15	ICD	1501	TGAGCTAAGAAGGATAATTGTCTTTTGGTAACTAGGTCTACAGGTTTACATTTTCTGTG
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	ICD	1621	TTTTCTATAAGTTTACAGCCTTTTCTTATATATACAGTTATTGCCACCTTTGTGAACAT
	IRT-4C1	531	-----
25	ICD	1681	GGCAAGGGACTTTTTTACAATTTTATTTTATTTTCTAGTACCAGCCTAGGAATTCGGTT
	IRT-4C1	531	-----
	ICD	1741	AGTACTCATTTGTATTCACTGTCACTTTTCTCATGTTCTAATTATAAATGACCAAAATC
	IRT-4C1	531	-----
30	ICD	1801	AAGATTGCTCAAAGGGTAAATGATAGCCACAGTATTGCTCCCTAAAATATGCATAAAGT
	IRT-4C1	531	-----
	ICD	1861	AGAAATTCAGTGCCTTCCCCTCCTGTCCATGACCTTGGGCACAGGGAAGTTCTGGTGTCA
35	IRT-4C1	531	-----
	ICD	1921	TAGATATCCCGTTTTGTGAGGTAGAGCTGTGCATTAACTTGCACATGACTGGAACGAAG
	IRT-4C1	531	-----
40	ICD	1981	TAGGAGTGCAACTCAAATGTGTTGAAGATACTGCAGTCATTTTGTAAAGACCTTGCTGA
	IRT-4C1	531	-----
	ICD	2041	ATGTTTCCAATAGACTAAATACTGTTTAGGCCGAGGAGAGTTTGAATCCGGAATAAAT
	IRT-4C1	531	-----
45	ICD	2101	ACTACCTGGAGGTTTGTCTCTCCATTTTCTCTTTCTCCTCCTGGCCTGGCCTGAATAT
	IRT-4C1	531	-----
	ICD	2161	TATACTACTCTAAATAGCATATTTTCATCCAAGTGCAATAATGTAAGCTGAATCTTTTTTG
50	IRT-4C1	531	-----
	ICD	2221	GACTTCTGCTGGCCTGTTTTATTCTTTTATATAAATGTGATTCTCAGAAATTGATATT
	IRT-4C1	531	-----
55	ICD	2281	AAACACTATCTTATCTTCTCTCTG
	IRT-4C1	531	-----

**Figure 6**  
**Alignment between IDH2 and IDH1 amino acid sequences**

5

Score = 584 bits (1505), Expect = e-165  
 Identities = 281/397 (70%), Positives = 328/397 (81%), Gaps = 2/397 (0%)

10



15

IDH2: 50 VVEMDGDDEMTRIIWQFIKEKLILPHVDIQLKYFDLGLPNRDQTDQVTIDSALATQKYSV 109  
 VVEM GDEMTRIIW+ IKEKLI P+V++ L +DLG+ NRD T+DQVT D+A A +K++V  
 IDH1: 10 VVEMQGDDEMTRIIWELIKEKLIFPYVELDLHSYDLGIENRDATNDQVTKDAAEAIAKKHNV 69

20

IDH2: 110 AVKCATITPDEARVEEFKLKMKWKS PNGTIRNILGGTVFREPIICKNIPRLVPGWTKPIT 169  
 VKCATITPDE RVEEFKLK+MWKS PNGTIRNILGGTVFRE IICKNIPRLV GW KPI  
 IDH1: 70 GVKCATITPDEKRVVEEFKLKQMWKS PNGTIRNILGGTVFREAIICKNIPRLVSGWVKPII 129

25

IDH2: 170 IGRHAHGDQYKATDFVADRAGTFKMVFETPKDGSVKEWEVYNFP-AGGVGMGMYN TDESI 228  
 IGRHA+GDQY+ATDFV G ++ +TP DG+ + V+NF GGV MGMYN D+SI  
 IDH1: 130 IGRHAYGDQYRATDFVVPGPVKVEITYTPSDGTQKVITYLVHNFEEGGVAMGMYNQDKSI 189

IDH2: 229 SGFAHSCFQYAIQKKWPLYMSTKNTILKAYDGRFKDIFQEIFDKHYKTDFDKNKIWEHR 288  
 FAHS FQ A+ K WPLY+STKNTILK YDGRFKDIFQEI+DK YK+ F+ KIWEHR  
 IDH1: 190 EDFAHSSFMALSKGWPLYLSTKNTILKKYDGRFKDIFQEIYDKQYKSQFEAQKIWEHR 249

30

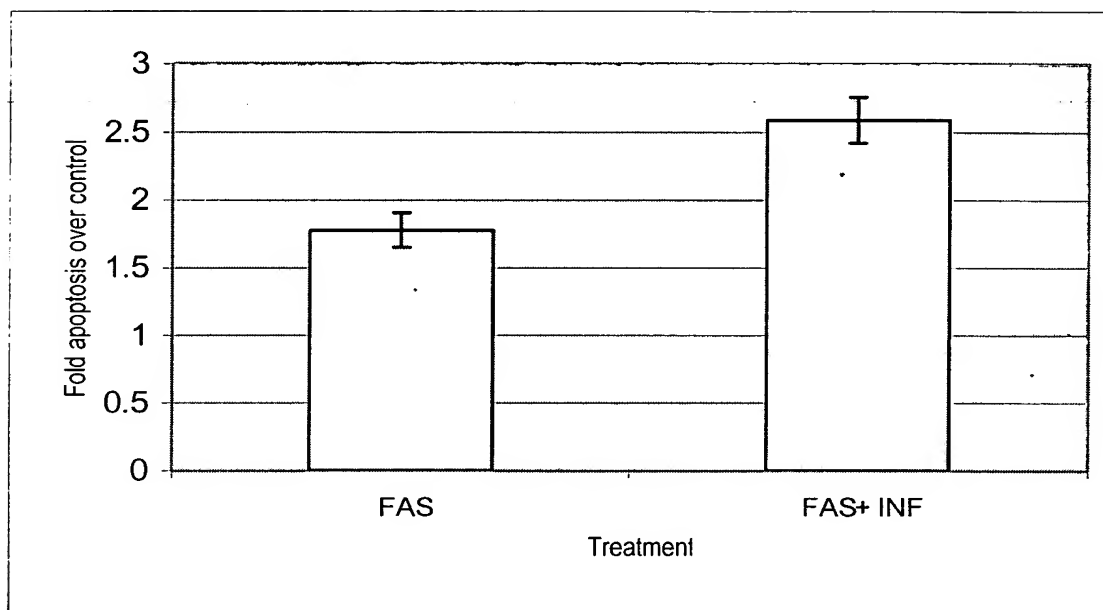
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 IDH1: 250 LIDDMVAQAMKSEGGFIWACKNYDGDVQSDSVAQGYGSLGMMTSVLVCPDGKTVEEAAH 309

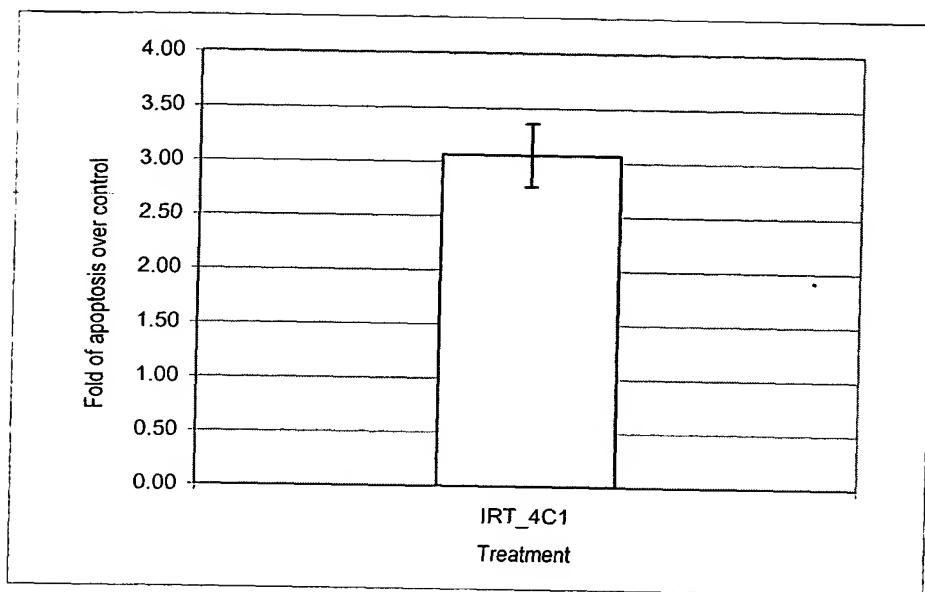
IDH2: 349 GTVTRHYREHQKRPTSTNPIASIFAWTRGLEHRGKLDGNQDLIRFAQMLEKVCVETVES 408  
 GTVTRHYR +QKG+ TSTNPIASIFAWTRGL HR KLD N++L FA LE+V +ET+E+  
 IDH1: 310 GTVTRHYRMYQKQETSTNPIASIFAWTRGLAHRKLDNNKELAFFANALEEVSIIETIEA 369

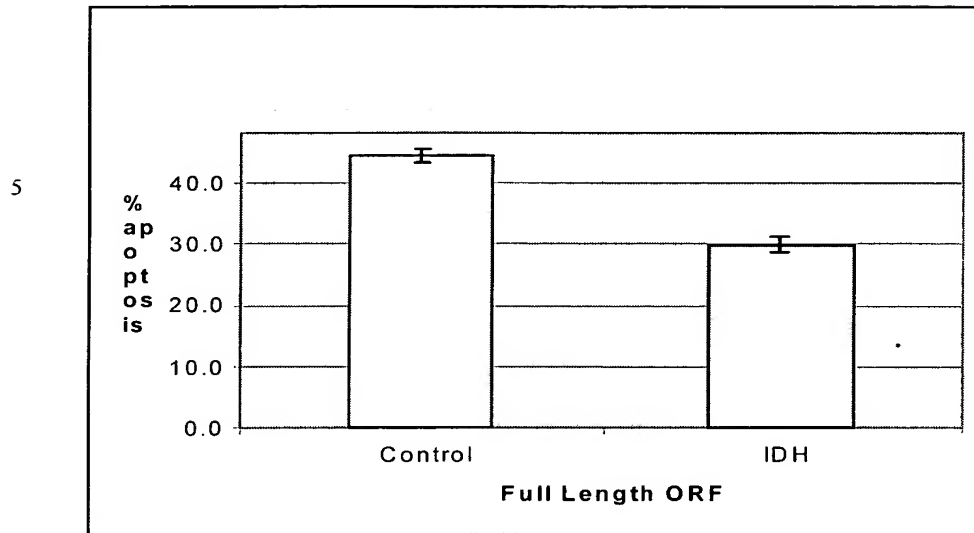
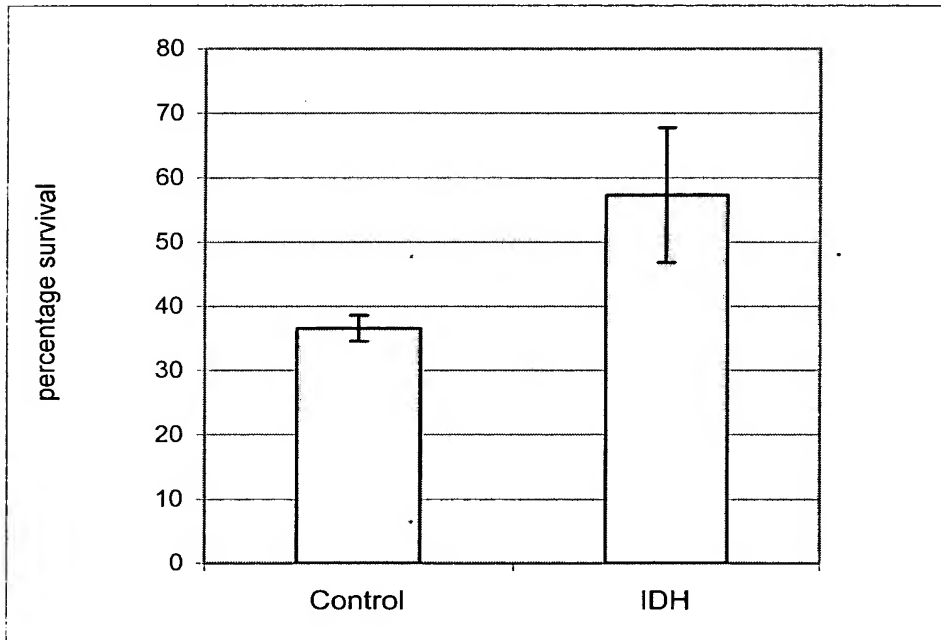
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IDH2: 409 GAMTKDLACIHLGLSNVKNLNEHFLNTTDFLDTIKSNL 445  
 G MTKDLA CI GL NV+ ++ +LNT +F+D + NL  
 IDH1: 370 GFMTKDLAACIKGLPNVQRSD-YLNTFEFMDKLGENL 405



**Figure 7**

**Figure 8**

**Figure 9****A) apoptosis protection****B) viability assay**

**Figure 10**